IN THE CLAIMS

The status of each claim is listed below.

Claims 1-54: Canceled.

55. (New) A quantitative polymorphous analysis method, comprising:

determining the initial concentration of a target gene;

amplifying a target gene and monitoring the amplification by real-time PCR,

wherein said determining and amplifying are conducted at the same time;

performing a polymorphous analysis with respect to the amplified target gene to determine a polymorphous composition ratio of individual components of the target gene; and

determining the initial amount of the target gene and an initial polymorphous composition of the target gene or initial amounts of individual components of the target gene.

56. (New) The method of Claim 55, wherein said real-time PCR is accomplished with a nucleic acid probe,

wherein the probe comprises a single-stranded oligonucleotide capable of hybridizing to the target nucleic gene,

wherein the probe is labeled with a fluorescent dye and a quencher substance,

wherein the oligonucleotide is labeled with the fluorescent dye and the quencher substance such that the intensity of fluorescence in a hybridization reaction system increases when the probe is hybridized with the target gene, and

wherein the oligonucleotide forms no stem-loop structure between bases at positions where the oligonucleotide is labeled with the fluorescent dye and the quencher substance.

57. (New) The method of Claim 55, wherein said real-time PCR is accomplished with a nucleic acid probe,

wherein said probe is labeled at an end portion thereof with said fluorescent dye, and

said probe has a base sequence designed such that, when said probe hybridizes at said end portion thereof to said target nucleic acid, at least one G (guanine) base exists in a base sequence of said target gene at a position 1 to 3 bases apart from an end base of said target nucleic acid hybridized with said probe;

whereby said fluorescent dye is reduced in fluorescence emission when said probe labeled with said fluorescent dye hybridizes to said target gene.

58. (New) The method of Claim 55, wherein said real-time PCR is accomplished with a nucleic acid probe,

wherein said probe is labeled at an end portion thereof with a fluorescent dye, and

wherein said probe has a base sequence designed such that, when said probe hybridizes to said target gene, plural base pairs in a probe-nucleic acid hybrid complex form at least one G (guanine) and C (cytosine) pair at said end portion;

whereby said fluorescent dye is reduced in fluorescence emission when said probe labeled with said fluorescent dye hybridizes to said target gene.

59. (New) The method of Claim 55, wherein said real-time PCR is accomplished with a nucleic acid probe,

wherein said probe is labeled with a fluorescent dye, wherein said probe is labeled at a modification portion other than a 5' end phosphate group or a 3' end OH group thereof with said fluorescent dye, and

wherein said probe has a base sequence designed such that, when said probe hybridizes to said target gene, plural base pairs in a probe-nucleic acid hybrid complex form at least one G (guanine) and C (cytosine) pair at said modification portion; whereby said fluorescent dye is reduced in fluorescence emission when said probe labeled with said fluorescent dye hybridizes to said target gene.

60. (New) The method of Claim 55, wherein said real-time PCR is accomplished with a nucleic acid probe, and determining an initial concentration of the amplified target gene from a percentage of a change in an intensity of fluorescence occurred as a result of hybridization between to said probe and said amplified target gene.

61. (New) The method of Claim 55, wherein said real-time PCR is accomplished with a nucleic acid probe, and including determining an initial concentration of the amplified target gene from a percentage of a change in an intensity of fluorescence occurred as a result of hybridization between said primer or an amplified nucleic acid amplified from said primer and said amplified target gene.

62. (New) The method of Claim 55, wherein said real-time PCR is accomplished with a nucleic acid probe, and including measuring an intensity of fluorescence in a reaction system in which said probe and said target gene or amplified nucleic acid have not hybridized with each other and also an intensity of fluorescence in said reaction system in which said probe and said target nucleic acid or amplified nucleic acid are hybridized with each other; and then calculating percentage of a decrease of said former intensity of fluorescence from said latter intensity of fluorescence.

63. (New) The method of Claim 56, further comprising correcting an intensity value of fluorescence in a reaction system, said intensity value being available after said target nucleic acid has hybridized to said nucleic acid probe labeled with said fluorescent dye, in accordance with an intensity value of fluorescence in said reaction system available after a probe-nucleic acid hybrid complex so formed has been denatured.

64. (New) The method of Claim 56, further comprising, as a correction processing step, correcting an intensity value of fluorescence in a reaction system, said intensity being available in each cycle after said amplified nucleic acid has conjugated to said fluorescent dye or after said amplified nucleic acid has hybridized to said nucleic acid probe labeled with said fluorescent dye, in accordance with an intensity value of fluorescence in said reaction system available after a nucleic acid-fluorescent dye conjugate or probe-nucleic acid hybrid complex so formed has been denatured in said cycle.

65. (New) The method of Claim 64, wherein said correction-processing step is performed in accordance with the following formula (1) or formula (2):

$fn = fhyb, n/fden,n$ (1)

$fn = f=fden, n/fhyb,n$ (2)

where

fn: correction-processed value in an nth cycle as calculated in accordance with the formula (1) or formula (2),

fhyb,n: intensity value of fluorescence of the reaction system available after said amplified nucleic acid has conjugated to said fluorescent dye or said amplified nucleic acid has hybridized to said nucleic acid probe labeled with said fluorescent dye in said nth cycle, and

fden,n: intensity value of fluorescence of the reaction system available after said formed fluorescent dye-nucleic acid conjugate or said formed probe-nucleic acid hybrid complex has dissociated in said nth cycle.

66. (New) The method of Claim 65, further comprising:

introducing correction-processed values which have been calculated in accordance with the formula (1) or formula (2) in individual cycles, into the following formula (3) or (4) to calculate rates or percentages of changes in fluorescence between samples in said individual cycles:

Fn = fn/fa (3)

Fn = fa/fn (4)

where

Fn: rate or percentage of a change in fluorescence in an nth cycle as calculated in accordance with the formula (3) or formula (4),

Fn: correction-processed value calculated in said nth cycle as calculated in accordance with the formula (1) or formula (2), and

fa: correction-processed value calculated in a given cycle before a change in fn is observed as calculated in accordance with the formula (1) or formula (2); and comparing said rates or percentages of changes in fluorescence.

67. (New) The method of Claim 65, further comprising:

1) performing processing in accordance with the following formula (5), (6) or (7) by using data of rates or percentages of changes in fluorescence as calculated in accordance with said formula (3) or (4):

logb(Fn), ln(Fn) (5)

$\log b\{(1-Fn) \times A\}$, $\ln\{(1-Fn) \times A\}$ (6)

$\log b\{(Fn-1) \times A\}$, $\ln\{(Fn-1) \times A\}$ (7)

where

A, b: desired numerical values, and

Fn: rate or percentage of a change in fluorescence in an nth cycle as calculated in accordance with the formula (3) or formula (4),

2) determining a cycle in which said processed value of said processing step 1) has reached a constant value,

3) calculating a relational expression between cycle of a nucleic acid sample of a known concentration and the number of copies of said target nucleic acid at the time of initiation of a reaction, and

4) determining the number of copies of said target nucleic acid in an unknown sample upon initiation of PCR.

68. (New) The method of Claim 55, wherein said polymorphous analysis is T-RELP (terminal restriction fragment length polymorphism), RFLP (restriction fragment length polymorphism), SSCP (single strand conformation) or CFLP (cleavage fragment length polymorphism).

69. (New) The method of Claim 55, wherein the polymorphous analysis is determined using a sequencer.

70. (New) The method of Claim 56, wherein said single-stranded oligonucleotide is labeled on the same nucleotide thereof with said fluorescent dye and said quencher substance.

71. (New) The method of Claim 56, wherein the distance between said bases at said positions where said oligonucleotide is labeled with said fluorescent dye and quencher substance, respectively, is 1 to 20.

72. (New) The method of claim 56, wherein said probe is labeled at a 3' end thereof with said fluorescent dye.

73. (New) The method of claim 56, wherein said probe is labeled at a 5' end thereof with said fluorescent dye.

74. (New) The method of claim 56, wherein said probe has G or C as a 3' end base and is labeled at said 3' end thereof with said fluorescent dye.

75. (New) The method of claim 56, wherein said probe has G or C as a 5' end base and is labeled at said 5' end thereof with said fluorescent dye.

76. (New) The method of claim 74, wherein a hydroxyl group on a 3' carbon of ribose or deoxyribose at said 3' end or a hydroxyl group on a 3' or 2' carbon of ribose at said 3' end has been phosphorylated.

77. (New) The method of claim 56, wherein said probe is labeled at a 5' end phosphate group and/or a 3' end phosphate group thereof with said fluorescent dye.

78. (New) The method of claim 56, wherein said oligonucleotide of said probe is a chemically-modified nucleic acid.

79. (New) The method of claim 78, wherein said chemically-modified nucleic acid is 2'-O-methyloligonucleotide, 2'-O-ethyloligonucleotide, 2'-O-butyloligonucleotide, 2'-O-ethylenecligonucleotide, or 2'-O-benzyl-oligonucleoatide.

80. (New) The method of claim 56, wherein said oligonucleotide of said probe is a chimeric oligonucleotide which comprises a ribonucleotide and a deoxyribonucleotide.

81. (New) The method of claim 80, wherein said chimeric oligonucleotide comprises 2'-O-methyloligonucleotide, 2'--ethyloligonucleotide, 2'-O-butyloligonucleotide 2'-O-ethyleneoligonucleotide, or 2'-O-benzyl-oligonucleotide.

SUPPORT FOR THE AMENDMENTS

The amendment to the substitute specification that were originally filed in the Preliminary Amendment on November 19, 2001 has been submitted herewith, expect that at page 66, "increase" has been replaced with –increase or decrease--. Support for all of the amendments is found in the substitute specification. In particular, the amendment at page 66 noted above is believed to be supported by the substitute specification at pages 6-7, where a decrease and an increase in emission are discussed.

Newly-added Claims 55-81 are supported by the substitute specification at pages and by original Claims 1-54.

No new matter is believed to have been added to the present application by the amendments submitted above.